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RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/837,235

TIME: 10:22:38

Input Set : A:\9725-005-999.txt

Output Set: N:\CRF3\08282001\I837235.raw

ENTERED

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5 <110> APPLICANT: Marshall, Christopher
7 Hoffman, Alexander
9 Errico, Joseph
11 Marshall, Paul
15 <120> TITLE OF INVENTION: STABILIZED PROTEINS
19 <130> FILE REFERENCE: 9725-005-999
23 <140> CURRENT APPLICATION NUMBER: 09/837,235
25 <141> CURRENT FILING DATE: 2001-04-18
29 <150> PRIOR APPLICATION NUMBER: PCT/US00/28595
31 <151> PRIOR FILING DATE: 2000-10-16
35 <150> PRIOR APPLICATION NUMBER: 60/159,763
37 <151> PRIOR FILING DATE: 1999-10-15
41 <160> NUMBER OF SEQ ID NOS: 42
45 <170> SOFTWARE: PatentIn version 3.0
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 954
53 <212> TYPE: DNA
55 <213> ORGANISM: Candida antarctica
59 <400> SEQUENCE: 1
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62 acctgccagg gtgcttcgcc atcctcgggc tccaaacca tccttctcgt ccccggaacc 120
64 ggcaccacag gtccacagtc gttcgactcg aactggatcc ccctctcaac gcagttgggt 180
66 tacacaccct gctggatctc acccccgccg ttcatgctca acgacacca ggtcaacacg 240
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70 gtgcttacct ggtcccaggg tggctctggt gcacagtggg gtctgacctt cttccccagt 360
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74 gccggccctc tcgatgcact cgcggttagt gcacctccg tatggcagca aaccaccggt 480
76 tcggcactca ccaccgcaact ccgaaacgca ggtggtctga cccagatcgt gccaccacc 540
78 aacctctact cggcgaccga cgagatcggt cagcctcagg tgtccaactc gccactcgac 600
80 tcatcctacc tcttcaacgg aaagaacgtc caggcacagg ccgtgtgtgg gccgctgttc 660
82 gtcacgacc atgcaggctc gtcacctcg cagttctcct acgtcgtcgg tcgatccgcc 720
84 ctgcgctcca ccacgggcca ggctcgtagt gcagactatg gcattacgga ctgcaaccct 780
86 cttcccgcca atgatctgac tcccgagcaa aaggctgccg cggctgcgct cctggcgccg 840
88 gcagctgcag ccacgtggc ggggtccaaag cagaactgcg agcccgaact catgccctac 900
90 gcccgccctt ttgcagtagg caaaaggacc tgctccggca tcgtcaccct ctga 954
93 <210> SEQ ID NO: 2
95 <211> LENGTH: 317
97 <212> TYPE: PRT
99 <213> ORGANISM: Candida antarctica
103 <400> SEQUENCE: 2
105 Leu Pro Ser Gly Ser Asp Pro Ala Phe Ser Gln Pro Lys Ser Val Leu
106 1 5 10 15
108 Asp Ala Gly Leu Thr Cys Gln Gly Ala Ser Pro Ser Ser Val Ser Lys
109 20 25 30
111 Pro Ile Leu Leu Val Pro Gly Thr Gly Thr Thr Gly Pro Gln Ser Phe
112 35 40 45
114 Asp Ser Asn Trp Ile Pro Leu Ser Thr Gln Leu Gly Tyr Thr Pro Cys

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115      50      55      60
117 Trp Ile Ser Pro Pro Pro Phe Met Leu Asn Asp Thr Gln Val Asn Thr
118 65      70      75      80
120 Glu Tyr Met Val Asn Ala Ile Thr Ala Leu Tyr Ala Gly Ser Gly Asn
121      85      90      95
123 Asn Lys Leu Pro Val Leu Thr Trp Ser Gln Gly Gly Leu Val Ala Gln
124      100      105      110
126 Trp Gly Leu Thr Phe Phe Pro Ser Ile Arg Ser Lys Val Asp Arg Leu
127      115      120      125
129 Met Ala Phe Ala Pro Asp Tyr Lys Gly Thr Val Leu Ala Gly Pro Leu
130      130      135      140
132 Asp Ala Leu Ala Val Ser Ala Pro Ser Val Trp Gln Gln Thr Thr Gly
133 145      150      155      160
135 Ser Ala Leu Thr Thr Ala Leu Arg Asn Ala Gly Gly Leu Thr Gln Ile
136      165      170      175
138 Val Pro Thr Thr Asn Leu Tyr Ser Ala Thr Asp Glu Ile Val Gln Pro
139      180      185      190
141 Gln Val Ser Asn Ser Pro Leu Asp Ser Ser Tyr Leu Phe Asn Gly Lys
142      195      200      205
144 Asn Val Gln Ala Gln Ala Val Cys Gly Pro Leu Phe Val Ile Asp His
145      210      215      220
147 Ala Gly Ser Leu Thr Ser Gln Phe Ser Tyr Val Val Gly Arg Ser Ala
148 225      230      235      240
150 Leu Arg Ser Thr Thr Gly Gln Ala Arg Ser Ala Asp Tyr Gly Ile Thr
151      245      250      255
153 Asp Cys Asn Pro Leu Pro Ala Asn Asp Leu Thr Pro Glu Gln Lys Val
154      260      265      270
156 Ala Ala Ala Ala Leu Leu Ala Pro Ala Ala Ala Ala Ile Val Ala Gly
157      275      280      285
159 Pro Lys Gln Asn Cys Glu Pro Asp Leu Met Pro Tyr Ala Arg Pro Phe
160      290      295      300
162 Ala Val Gly Lys Arg Thr Cys Ser Gly Ile Val Thr Pro
163 305      310      315

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165 <210> SEQ ID NO: 3

167 <211> LENGTH: 57

169 <212> TYPE: DNA

171 <213> ORGANISM: Candida antarctica

175 <400> SEQUENCE: 3

176 atgggaattc catcatcatc atcatcacag cagcggccta ccttccggtt cggaccc

57

179 <210> SEQ ID NO: 4

181 <211> LENGTH: 37

183 <212> TYPE: DNA

185 <213> ORGANISM: Candida antarctica

189 <400> SEQUENCE: 4

190 ctcttggcgg ccgcctatca gggggtgacg atgccgg

37

193 <210> SEQ ID NO: 5

195 <211> LENGTH: 68

197 <212> TYPE: DNA

199 <213> ORGANISM: Candida antarctica

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203 <400> SEQUENCE: 5
204 atgggaattc catcatcatc atcatcacag cagcggccta ccttcgggtt cggaccctgc      60
206 ctattcgc                                                                    68
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211 <211> LENGTH: 24
213 <212> TYPE: DNA
215 <213> ORGANISM: Candida antarctica
219 <400> SEQUENCE: 6
220 cgactcgaac tacatcccc tctc                                              24
223 <210> SEQ ID NO: 7
225 <211> LENGTH: 24
227 <212> TYPE: DNA
229 <213> ORGANISM: Candida antarctica
233 <400> SEQUENCE: 7
234 gagaggggga tgtagttcga gtcg                                              24
237 <210> SEQ ID NO: 8
239 <211> LENGTH: 25
241 <212> TYPE: DNA
243 <213> ORGANISM: Candida antarctica
247 <400> SEQUENCE: 8
248 ggggtctgacc tacttccccca gtatc                                          25
251 <210> SEQ ID NO: 9
253 <211> LENGTH: 25
255 <212> TYPE: DNA
257 <213> ORGANISM: Candida antarctica
261 <400> SEQUENCE: 9
262 gatactgggg aagtaggtca gaccc                                           25
265 <210> SEQ ID NO: 10
267 <211> LENGTH: 21
269 <212> TYPE: DNA
271 <213> ORGANISM: Candida antarctica
275 <400> SEQUENCE: 10
276 cgatgagatt tccttcaatt t                                              21
279 <210> SEQ ID NO: 11
281 <211> LENGTH: 21
283 <212> TYPE: DNA
285 <213> ORGANISM: Candida antarctica
289 <400> SEQUENCE: 11
290 tctagaaagg tggcggccgc c                                              21
293 <210> SEQ ID NO: 12
295 <211> LENGTH: 22
297 <212> TYPE: DNA
299 <213> ORGANISM: Candida antarctica
303 <400> SEQUENCE: 12
304 gaagctggat tccatcatca tc                                              22
307 <210> SEQ ID NO: 13
309 <211> LENGTH: 21
311 <212> TYPE: DNA
313 <213> ORGANISM: Candida antarctica

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317 <400> SEQUENCE: 13
318 tctagaaagg tggcggccgc c 21
321 <210> SEQ ID NO: 14
323 <211> LENGTH: 1074
325 <212> TYPE: DNA
327 <213> ORGANISM: Bacillus subtilis
331 <400> SEQUENCE: 14
332 atgtctgtgc aggctgccgg aaaaagcagt acagaaaaga aatacattgt cggatttaaa 60
334 cagacaatga gtgccatgag ttccgccaaag aaaaaggatg ttatttctga aaaaggcgga 120
336 aaggttcaaa agcaatttaa gtatgttaac gcggccgcag caacattgga tgaaaaagct 180
338 gtaaaagaat tgaaaaaaga tccgagcggt gcatatgtgg aagaagatca tattgcacat 240
340 gaatatgcgc aatctgttcc ttatggcatt tctcaaatta aagcgccggc tcttcactct 300
342 caaggctaca caggctctaa cgtaaaagta gctgttatcg acagcggaat tgactcttct 360
344 catcctgact taaacgtcag aggcgaggca agcttcgtac cttctgaaac aaaccatac 420
346 caggacggca gttctcacgg tacgcatgta gccggtacga ttgccgtctt taataactca 480
348 atcgggtgtt tgggcggttag cccaagcgca tcattatatg cagtaaaagt gcttgattca 540
350 acaggaagcg gccaatatag ctggattatt aacggcattg agtgggccat ttccaacaat 600
352 atggatgta tcaacatgag ccttggcgga cctactggtt ctacagcgct gaaaacagtc 660
354 gttgacaaaag ccgtttccag cggtatcgct gttgctgccg cagccggaaa cgaagggttca 720
356 tccggaagca caagcacagt cggctaccct gcaaaatata cttctactat tgcagtaggt 780
358 gcggtaaaaca gcagcaacca aagagcttca ttctccagcg caggttctga gcttgatgtg 840
360 atggctcctg gcgtgtccat ccaaagcaca ctctcgtggag gcacttacgg cgcttataac 900
362 ggaacgtcca tggcgactcc tcacgttgcc ggagcagcag cgtaatttct ttctaagcac 960
364 ccgacttga caaacgcgca agtccgtgat cgtttagaaa gcactgcaac atatcttgga 1020
366 aactctttct actatggaaa agggttaatc aacgtacaag cagctgcaca ataa 1074
369 <210> SEQ ID NO: 15
371 <211> LENGTH: 357
373 <212> TYPE: PRT
375 <213> ORGANISM: Bacillus subtilis
379 <400> SEQUENCE: 15
381 Met Ser Val Gln Ala Ala Gly Lys Ser Ser Thr Glu Lys Lys Tyr Ile
382 1 5 10 15
384 Val Gly Phe Lys Gln Thr Met Ser Ala Met Ser Ser Ala Lys Lys Lys
385 20 25 30
387 Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln Phe Lys Tyr
388 35 40 45
390 Val Asn Ala Ala Ala Thr Leu Asp Glu Lys Ala Val Lys Glu Leu
391 50 55 60
393 Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His Ile Ala His
394 65 70 75 80
396 Glu Tyr Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro
397 85 90 95
399 Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val
400 100 105 110
402 Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly
403 115 120 125
405 Gly Ala Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser
406 130 135 140
408 Ser His Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser

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409 145                               150                               155                               160
411 Ile Gly Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys
412                               165                               170                               175
414 Val Leu Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly
415                               180                               185                               190
417 Ile Glu Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu
418                               195                               200                               205
420 Gly Gly Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala
421                               210                               215                               220
423 Val Ser Ser Gly Ile Val Val Ala Ala Ala Gly Asn Glu Gly Ser
424 225                               230                               235                               240
426 Ser Gly Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr
427                               245                               250                               255
429 Ile Ala Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser
430                               260                               265                               270
432 Ser Ala Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln
433                               275                               280                               285
435 Ser Thr Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met
436                               290                               295                               300
438 Ala Thr Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His
439 305                               310                               315                               320
441 Pro Thr Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala
442                               325                               330                               335
444 Thr Tyr Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val
445                               340                               345                               350
447 Gln Ala Ala Ala Gln
448                               355
450 <210> SEQ ID NO: 16
452 <211> LENGTH: 269
454 <212> TYPE: PRT
456 <213> ORGANISM: Bacillus subtilis
460 <400> SEQUENCE: 16
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463 1                               5                               10                               15
465 His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
466                               20                               25                               30
468 Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
469                               35                               40                               45
471 Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
472                               50                               55                               60
474 His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
475 65                               70                               75                               80
477 Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
478                               85                               90                               95
480 Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
481                               100                              105                              110
483 Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
484                               115                              120                              125
486 Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly

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VERIFICATION SUMMARY

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